



SEQUENCE LISTING

<110> Yamamoto, Hiroshi
Kimoto, Norihiro

<120> NOVEL ENONE REDUCTASES, METHODS FOR
PRODUCING SAME, AND METHODS FOR SELECTIVELY REDUCING A
CARBON-CARBON DOUBLE BOND OF AN ALPHA,BETA-UNSATURATED KETONE
USING THE REDUCTASES

<130> 06501-100001

<140> US 10/081,644

<141> 2002-02-21

<150> JP 2001-49363

<151> 2001-02-23

<160> 29

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1113

<212> DNA

<213> Kluyveromyces lactis

<220>

<221> CDS

<222> (1)...(1110)

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1 5 10 15

gct gtt gtt aaa aca gat gtc tca gtt cca gaa tta aag gag ggt aca 96
Ala Val Val Lys Thr Asp Val Ser Val Pro Glu Leu Lys Glu Gly Thr
20 25 30

gcc ttg gtg aag gtt gag gct gtt gct ggt aac cca act gat tgg aag 144
Ala Leu Val Lys Val Glu Ala Val Ala Gly Asn Pro Thr Asp Trp Lys
35 40 45

cat att gct tat aag att ggt cca gaa ggt tca att cta gga tgt gac 192
His Ile Ala Tyr Lys Ile Gly Pro Glu Gly Ser Ile Leu Gly Cys Asp
50 55 60

att gct ggt aca gtt gtc aaa ctt gga cca aat gct agt act gac ttg 240
Ile Ala Gly Thr Val Val Lys Leu Gly Pro Asn Ala Ser Thr Asp Leu
65 70 75 80

aag gtt gga gat acc ggt ttc ggt ttt gtt cac ggt gct tcc caa aca 288
Lys Val Gly Asp Thr Gly Phe Gly Phe Val His Gly Ala Ser Gln Thr
85 90 95

gat cct aaa aat ggt gca ttt gct gaa tat gcc agg gtt tat cca cct 336
 Asp Pro Lys Asn Gly Ala Phe Ala Glu Tyr Ala Arg Val Tyr Pro Pro 110
 100 105

ttg ttt tac aag agt aac tta act cac tca act gct gat gaa att tct 384
 Leu Phe Tyr Lys Ser Asn Leu Thr His Ser Thr Ala Asp Glu Ile Ser 125
 115 120

gaa ggc cct gtg aag aac ttc gaa tct gct gca tca ttg cca gtt tcg 432
 Glu Gly Pro Val Lys Asn Phe Glu Ser Ala Ala Ser Leu Pro Val Ser 140
 130 135

ttg aca act gct ggt gtt agt ttg tgt cat cac ttg ggc tca aaa atg 480
 Leu Thr Thr Ala Gly Val Ser Leu Cys His His Leu Gly Ser Lys Met 160
 145 150 155

gaa tgg cac cca tct acc ccg caa cat act cat cca tta ttg att tgg 528
 Glu Trp His Pro Ser Thr Pro Gln His Thr His Pro Leu Leu Ile Trp 175
 165 170

ggt ggt gct aca gca gtg ggt caa caa cta atc caa gtt gcc aaa cat 576
 Gly Gly Ala Thr Ala Val Gly Gln Leu Ile Gln Val Ala Lys His 190
 180 185

atc aat gct tat act aag att gta act gtt gct tct aaa aag cat gaa 624
 Ile Asn Ala Tyr Thr Lys Ile Val Thr Val Ala Ser Lys Lys His Glu 205
 195 200

aag ctt tta aag tct tat ggt gct gat gat gtc ttt gac tat cat gat 672
 Lys Leu Leu Lys Ser Tyr Gly Ala Asp Asp Val Phe Asp Tyr His Asp 220
 210 215

gca ggc gtt att gag cag atc aaa tcg aag tat cca aac ctg caa cat 720
 Ala Gly Val Ile Glu Gln Ile Lys Ser Lys Tyr Pro Asn Leu Gln His 240
 225 230 235

gtt att gac gct gtg gga agc gaa gat agt atc ccc gag gcc tat aaa 768
 Val Ile Asp Ala Val Gly Ser Glu Asp Ser Ile Pro Glu Ala Tyr Lys 255
 245 250

gtc aca gca gat agt cta cct gcc aca tta tta gaa gtg gtt cca atg 816
 Val Thr Ala Asp Ser Leu Pro Ala Thr Leu Leu Glu Val Val Pro Met 270
 260 265

acc att gaa agc att cct gaa gaa atc aga aaa gat aat gtt aaa att 864
 Thr Ile Glu Ser Ile Pro Glu Glu Ile Arg Lys Asp Asn Val Lys Ile 285
 275 280

gat att act ttg ttg tat cgt gca tct ggt caa gaa att cta ttg ggt 912
 Asp Ile Thr Leu Leu Tyr Arg Ala Ser Gly Gln Glu Ile Leu Leu Gly 300
 290 295

gca aca aga ttt cct gct agt cca gaa tat cat gaa gcc aca gtt aaa 960
 Ala Thr Arg Phe Pro Ala Ser Pro Glu Tyr His Glu Ala Thr Val Lys 320
 305 310

ttc gtt aag ttt ata aat cca cac ctt aac aac ggt gat atc cat cat 1008

Phe Val Lys Phe Ile Asn Pro His Leu Asn Asn Gly Asp Ile His His
 325 330 335
 atg aat att aaa gtt ttc agc aac ggc tta gat gat gtc cca gct ctc
 Met Asn Ile Lys Val Phe Ser Asn Gly Leu Asp Asp Val Pro Ala Leu
 340 345 350
 act gaa ggt ata aaa gaa ggt aaa aac aaa aat gtt aag tat gtt gcc
 Thr Glu Gly Ile Lys Glu Gly Lys Asn Lys Asn Val Lys Tyr Val Ala
 355 360 365
 agg tta taa
 Arg Leu
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<210> 2
 <211> 370
 <212> PRT
 <213> Kluyveromyces lactis

A2
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 20 25 30
 Ala Leu Val Lys Val Glu Ala Val Ala Gly Asn Pro Thr Asp Trp Lys
 35 40 45
 His Ile Ala Tyr Lys Ile Gly Pro Glu Gly Ser Ile Leu Gly Cys Asp
 50 55 60
 Ile Ala Gly Thr Val Val Lys Leu Gly Pro Asn Ala Ser Thr Asp Leu
 65 70 75 80
 Lys Val Gly Asp Thr Gly Phe Gly Phe Val His Gly Ala Ser Gln Thr
 85 90 95
 Asp Pro Lys Asn Gly Ala Phe Ala Glu Tyr Ala Arg Val Tyr Pro Pro
 100 105 110
 Leu Phe Tyr Lys Ser Asn Leu Thr His Ser Thr Ala Asp Glu Ile Ser
 115 120 125
 Glu Gly Pro Val Lys Asn Phe Glu Ser Ala Ala Ser Leu Pro Val Ser
 130 135 140
 Leu Thr Thr Ala Gly Val Ser Leu Cys His His Leu Gly Ser Lys Met
 145 150 155 160
 Glu Trp His Pro Ser Thr Pro Gln His Thr His Pro Leu Leu Ile Trp
 165 170 175
 Gly Gly Ala Thr Ala Val Gly Gln Gln Leu Ile Gln Val Ala Lys His
 180 185 190
 Ile Asn Ala Tyr Thr Lys Ile Val Thr Val Ala Ser Lys Lys His Glu
 195 200 205
 Lys Leu Leu Lys Ser Tyr Gly Ala Asp Asp Val Phe Asp Tyr His Asp
 210 215 220
 Ala Gly Val Ile Glu Gln Ile Lys Ser Lys Tyr Pro Asn Leu Gln His
 225 230 235 240
 Val Ile Asp Ala Val Gly Ser Glu Asp Ser Ile Pro Glu Ala Tyr Lys
 245 250 255
 Val Thr Ala Asp Ser Leu Pro Ala Thr Leu Leu Glu Val Val Pro Met
 260 265 270
 Thr Ile Glu Ser Ile Pro Glu Glu Ile Arg Lys Asp Asn Val Lys Ile

275
 Asp Ile Thr Leu Leu Tyr Arg Ala Ser Gly Gln Glu Ile Leu Leu Gly
 290
 Ala Thr Arg Phe Pro Ala Ser Pro Glu Tyr His Glu Ala Thr Val Lys
 305
 Phe Val Lys Phe Ile Asn Pro His Leu Asn Asn Gly Asp Ile His His
 310
 Met Asn Ile Lys Val Phe Ser Asn Gly Leu Asp Asp Val Pro Ala Leu
 325
 Thr Glu Gly Ile Lys Glu Gly Lys Asn Lys Asn Val Lys Tyr Val Ala
 340
 355
 Arg Leu
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<210> 3
 <211> 1145
 <212> DNA
 <213> *Saccharomyces cerevisiae*

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 <222> (6)...(1133)

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aat gcc aag gct gta gtc aaa cag gac att cca att cct gaa tta gaa
 Asn Gly Lys Ala Val Val Lys Gln Asp Ile Pro Ile Pro Glu Leu Glu
 20 25 30

gaa gga ttt gtt cta att aag act gtc gcc gtt gcc ggt aac cct acc
 Glu Gly Phe Val Leu Ile Lys Thr Val Ala Val Ala Gly Asn Pro Thr
 35 40 45

gat tgg aaa cat att gat ttc aag att ggt cct caa ggt gcc ctc tta
 Asp Trp Lys His Ile Asp Phe Lys Ile Gly Pro Gln Gly Ala Leu Leu
 50 55 60

ggc tgt gat gca gcc ggc caa atc gta aag ttg ggc cca aat gtt gat
 Gly Cys Asp Ala Ala Gly Gln Ile Val Lys Leu Gly Pro Asn Val Asp
 65 70 75

gct gca cgc ttt gcc att ggt gat tac att tat ggg gtt att cac ggt
 Ala Ala Arg Phe Ala Ile Gly Asp Tyr Ile Tyr Gly Val Ile His Gly
 80 85 90 95

gct tca gtg agg ttc ccc tca aac ggt gcc ttt gct gag tac tct gcc
 Ala Ser Val Arg Phe Pro Ser Asn Gly Ala Phe Ala Glu Tyr Ser Ala
 100 105 110

att tca tcc gag act gct tat aaa cca gcc aga gag ttt aga ttg tgc
 Ile Ser Ser Glu Thr Ala Tyr Lys Pro Ala Arg Glu Phe Arg Leu Cys
 115 120 125

ggt aaa gac aag cta cca gaa ggc ccc gta aaa tct tta gaa ggg gca

Gly Lys Asp Lys Leu Pro Glu Gly Pro Val Lys Ser Leu Glu Gly Ala
 130 135 140

gta tcc ctc cca gtc tca ttg acc acg gct ggt atg atc ctt aca cat
 Val Ser Leu Pro Val Ser Leu Thr Thr Ala Gly Met Ile Leu Thr His
 145 150 155 482

agt ttt ggc ttg gac atg aca tgg aag ccc tcc aaa gcg caa aga gat
 Ser Phe Gly Leu Asp Met Thr Trp Lys Pro Ser Lys Ala Gln Arg Asp
 160 165 170 530

caa ccc atc tta ttt tgg ggt ggc act gct gtt ggc cag atg ctt
 Gln Pro Ile Leu Phe Trp Gly Gly Ala Thr Ala Val Gly Gln Met Leu
 180 185 190 578

att caa ttg gca aaa aaa cta aac ggt ttc agc aag atc atc gtc gtt
 Ile Gln Leu Ala Lys Lys Leu Asn Gly Phe Ser Lys Ile Ile Val Val
 195 200 205 626

gct tct cgt aaa cat gaa aaa ttg ttg aaa gag tac ggt gca gat gaa
 Ala Ser Arg Lys His Glu Lys Leu Leu Lys Glu Tyr Gly Ala Asp Glu
 210 215 220 674

ctt ttt gac tac cac gat gct gac gtt atc gaa cag ata aaa aag aag
 Leu Phe Asp Tyr His Asp Ala Asp Val Ile Glu Gln Ile Lys Lys Lys
 225 230 235 722

tac aac aac att cct tac ttg gtg gac tgt gtc tcc aac aca gaa act
 Tyr Asn Asn Ile Pro Tyr Leu Val Asp Cys Val Ser Asn Thr Glu Thr
 240 245 250 770

att caa cag gtg tac aaa tgt gcc gct gat gac tta gac gct acg gtc
 Ile Gln Gln Val Tyr Lys Cys Ala Ala Asp Asp Leu Asp Ala Thr Val
 260 265 270 818

gtt caa ttg acc gtt tta acc gaa aaa gat atc aag gag gaa gac agg
 Val Gln Leu Thr Val Leu Thr Glu Lys Asp Ile Lys Glu Glu Asp Arg
 275 280 285 866

agg caa aac gtc agt att gaa gga acc ctt cta tat ttg ata gga ggt
 Arg Gln Asn Val Ser Ile Glu Gly Thr Leu Leu Tyr Leu Ile Gly Gly
 290 295 300 914

aac gac gtc cca ttt ggc acg ttt act ttg cca gca gac cct gaa tac
 Asn Asp Val Pro Phe Gly Thr Phe Thr Leu Pro Ala Asp Pro Glu Tyr
 305 310 315 962

aag gaa gcc gcc ata aaa ttt att aag ttc atc aat cca aaa atc aat
 Lys Glu Ala Ala Ile Lys Phe Ile Lys Phe Ile Asn Pro Lys Ile Asn
 320 325 330 1010

gat ggt gaa atc cac cac atc cca gtg aaa gtt tac aag aac ggg tta
 Asp Gly Glu Ile His His Ile Pro Val Lys Val Tyr Lys Asn Gly Leu
 340 345 350 1058

gat gat atc cca cag tta ctt gat gat att aag cac ggg agg aat tct
 Asp Asp Ile Pro Gln Leu Leu Asp Asp Ile Lys His Gly Arg Asn Ser
 1106

355

360

365

ggc gaa aag ttg gtt gcc gtc ttg aaa taatctagac tg
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 370 375

1145

<210> 4

<211> 376

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 4

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 Gly Lys Ala Val Val Lys Gln Asp Ile Pro Ile Pro Glu Leu Glu Glu
 20 25 30
 Gly Phe Val Leu Ile Lys Thr Val Ala Val Ala Gly Asn Pro Thr Asp
 35 40 45
 Trp Lys His Ile Asp Phe Lys Ile Gly Pro Gln Gly Ala Leu Leu Gly
 50 55 60
 Cys Asp Ala Ala Gly Gln Ile Val Lys Leu Gly Pro Asn Val Asp Ala
 65 70 75 80
 Ala Arg Phe Ala Ile Gly Asp Tyr Ile Tyr Gly Val Ile His Gly Ala
 85 90 95
 Ser Val Arg Phe Pro Ser Asn Gly Ala Phe Ala Glu Tyr Ser Ala Ile
 100 105 110
 Ser Ser Glu Thr Ala Tyr Lys Pro Ala Arg Glu Phe Arg Leu Cys Gly
 115 120 125
 Lys Asp Lys Leu Pro Glu Gly Pro Val Lys Ser Leu Glu Gly Ala Val
 130 135 140
 Ser Leu Pro Val Ser Leu Thr Thr Ala Gly Met Ile Leu Thr His Ser
 145 150 155 160
 Phe Gly Leu Asp Met Thr Trp Lys Pro Ser Lys Ala Gln Arg Asp Gln
 165 170 175
 Pro Ile Leu Phe Trp Gly Gly Ala Thr Ala Val Gly Gln Met Leu Ile
 180 185 190
 Gln Leu Ala Lys Lys Leu Asn Gly Phe Ser Lys Ile Ile Val Val Ala
 195 200 205
 Ser Arg Lys His Glu Lys Leu Leu Lys Glu Tyr Gly Ala Asp Glu Leu
 210 215 220
 Phe Asp Tyr His Asp Ala Asp Val Ile Glu Gln Ile Lys Lys Lys Tyr
 225 230 235 240
 Asn Asn Ile Pro Tyr Leu Val Asp Cys Val Ser Asn Thr Glu Thr Ile
 245 250 255
 Gln Gln Val Tyr Lys Cys Ala Ala Asp Asp Leu Asp Ala Thr Val Val
 260 265 270
 Gln Leu Thr Val Leu Thr Glu Lys Asp Ile Lys Glu Glu Asp Arg Arg
 275 280 285
 Gln Asn Val Ser Ile Glu Gly Thr Leu Leu Tyr Leu Ile Gly Gly Asn
 290 295 300
 Asp Val Pro Phe Gly Thr Phe Thr Leu Pro Ala Asp Pro Glu Tyr Lys
 305 310 315 320
 Glu Ala Ala Ile Lys Phe Ile Lys Phe Ile Asn Pro Lys Ile Asn Asp
 325 330 335
 Gly Glu Ile His His Ile Pro Val Lys Val Tyr Lys Asn Gly Leu Asp
 340 345 350

A2

Asp Ile Pro Gln Leu Leu Asp Asp Ile Lys His Gly Arg Asn Ser Gly
 355 360 365
 Glu Lys Leu Val Ala Val Leu Lys
 370 375

<210> 5
 <211> 1134
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
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 <222> (1)...(1131)

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gac ggt aaa gcg gtt gtt aaa gag ggc att ccc att cct gaa ttg gaa 96
 Asp Gly Lys Ala Val Val Lys Glu Gly Ile Pro Ile Pro Glu Leu Glu 30
 20 25

A2
 gaa gga ttc gta ttg att aag aca ctc gct gtt gct ggt aac ccc act 144
 Glu Gly Phe Val Leu Ile Lys Thr Leu Ala Val Ala Gly Asn Pro Thr 45
 35 40

gat tgg gca cac att gac tac aag atc ggg cct caa gga tct att ctg 192
 Asp Trp Ala His Ile Asp Tyr Lys Ile Gly Pro Gln Gly Ser Ile Leu 60
 50 55

gga tgt gat gct gct ggc caa att gtc aaa ttg ggc cca gct gtc aat 240
 Gly Cys Asp Ala Ala Gly Gln Ile Val Lys Leu Gly Pro Ala Val Asn 80
 65 70 75

cct aaa gac ttt tct atc ggt gat tat att tat ggg ttc att cac gga 288
 Pro Lys Asp Phe Ser Ile Gly Asp Tyr Ile Tyr Gly Phe Ile His Gly 95
 85 90

tct tcc gta agg ttt cct tcc aat ggt gct ttt gct gaa tat tct gct 336
 Ser Ser Val Arg Phe Pro Ser Asn Gly Ala Phe Ala Glu Tyr Ser Ala 110
 100 105

att tca act gtg gtt gcc tac aaa tca ccc aat gaa ctc aaa ttt ttg 384
 Ile Ser Thr Val Val Ala Tyr Lys Ser Pro Asn Glu Leu Lys Phe Leu 125
 115 120

ggt gag gat gtt cta cct gcc ggc cct gtc agg tct ttg gaa ggt gta 432
 Gly Glu Asp Val Leu Pro Ala Gly Pro Val Arg Ser Leu Glu Gly Val 140
 130 135

gcc act atc cca gtg tca ctg acc aca gcc ggc ttg gtg ttg acc tat 480
 Ala Thr Ile Pro Val Ser Leu Thr Thr Ala Gly Leu Val Leu Thr Tyr 160
 145 150 155

aac ttg ggc ttg gac ctg aag tgg gag cca tca acc cca caa aga aaa 528
 Asn Leu Gly Leu Asp Leu Lys Trp Glu Pro Ser Thr Pro Gln Arg Lys

165	170	175	
ggc ccc atc tta tta tgg ggc ggt gca act gca gta ggt cag tcg ctc Gly Pro Ile Leu Leu Trp Gly Gly Ala Thr Ala Val Gly Gln Ser Leu 180 185 190			576
atc caa tta gcc aat aaa ttg aat ggc ttc acc aag atc att gtt gtg Ile Gln Leu Ala Asn Lys Leu Asn Gly Phe Thr Lys Ile Ile Val Val 195 200 205			624
gct tct cgg aag cac gaa aaa ctt ttg aaa gaa tat ggt gct gat gaa Ala Ser Arg Lys His Glu Lys Leu Leu Lys Glu Tyr Gly Ala Asp Glu 210 215 220			672
tta ttt gat tat cat gat att gac gtg gta gaa caa att aaa cac aag Leu Phe Asp Tyr His Asp Ile Asp Val Val Glu Gln Ile Lys His Lys 225 230 235 240			720
tac aac aat atc tcg tat tta gtc gac tgt gtc gcg aat caa gat acg Tyr Asn Asn Ile Ser Tyr Leu Val Asp Cys Val Ala Asn Gln Asp Thr 245 250 255			768
ctt caa caa gtg tac aaa tgt gcg gcc gat aaa cag gat gct aca att Leu Gln Gln Val Tyr Lys Cys Ala Ala Asp Lys Gln Asp Ala Thr Ile 260 265 270			816
gtt gaa tta aaa aat ttg aca gaa gaa aac gtc aaa aaa gag aac agg Val Glu Leu Lys Asn Leu Thr Glu Glu Asn Val Lys Lys Glu Asn Arg 275 280 285			864
aga caa aac gtt act att gac ata ata agg cta tat tca ata ggt ggc Arg Gln Asn Val Thr Ile Asp Ile Ile Arg Leu Tyr Ser Ile Gly Gly 290 295 300			912
cat gaa gta cca ttt gga aac att act tta cca gcc gac tca gaa gct His Glu Val Pro Phe Gly Asn Ile Thr Leu Pro Ala Asp Ser Glu Ala 305 310 315 320			960
agg aaa gct gca ata aaa ttt atc aaa ttc atc aat cca aag att aat Arg Lys Ala Ala Ile Lys Phe Ile Lys Phe Ile Asn Pro Lys Ile Asn 325 330 335			1008
gat gga caa att cgc cat att cca gta agg gtc tat aag aac ggg ctt Asp Gly Gln Ile Arg His Ile Pro Val Arg Val Tyr Lys Asn Gly Leu 340 345 350			1056
tgt gat gtt cct cat atc cta aaa gac atc aaa tat ggt aag aac tct Cys Asp Val Pro His Ile Leu Lys Asp Ile Lys Tyr Gly Lys Asn Ser 355 360 365			1104
ggg gaa aaa ctc gtt gcc gta tta aac taa Gly Glu Lys Leu Val Ala Val Leu Asn 370 375			1134

<210> 6

<211> 377

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 6

Met Ala Gln Val Ala Ile Pro Glu Thr Met Lys Ala Val Val Ile Glu
 1 5 10 15
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 20 25 30
 Glu Gly Phe Val Leu Ile Lys Thr Leu Ala Val Ala Gly Asn Pro Thr
 35 40 45
 Asp Trp Ala His Ile Asp Tyr Lys Ile Gly Pro Gln Gly Ser Ile Leu
 50 55 60
 Gly Cys Asp Ala Ala Gly Gln Ile Val Lys Leu Gly Pro Ala Val Asn
 65 70 75 80
 Pro Lys Asp Phe Ser Ile Gly Asp Tyr Ile Tyr Gly Phe Ile His Gly
 85 90 95
 Ser Ser Val Arg Phe Pro Ser Asn Gly Ala Phe Ala Glu Tyr Ser Ala
 100 105 110
 Ile Ser Thr Val Val Ala Tyr Lys Ser Pro Asn Glu Leu Lys Phe Leu
 115 120 125
 Gly Glu Asp Val Leu Pro Ala Gly Pro Val Arg Ser Leu Glu Gly Val
 130 135 140
 Ala Thr Ile Pro Val Ser Leu Thr Thr Ala Gly Leu Val Leu Thr Tyr
 145 150 155 160
 Asn Leu Gly Leu Asp Leu Lys Trp Glu Pro Ser Thr Pro Gln Arg Lys
 165 170 175
 Gly Pro Ile Leu Leu Trp Gly Gly Ala Thr Ala Val Gly Gln Ser Leu
 180 185 190
 Ile Gln Leu Ala Asn Lys Leu Asn Gly Phe Thr Lys Ile Ile Val Val
 195 200 205
 Ala Ser Arg Lys His Glu Lys Leu Leu Lys Glu Tyr Gly Ala Asp Glu
 210 215 220
 Leu Phe Asp Tyr His Asp Ile Asp Val Val Glu Gln Ile Lys His Lys
 225 230 235 240
 Tyr Asn Asn Ile Ser Tyr Leu Val Asp Cys Val Ala Asn Gln Asp Thr
 245 250 255
 Leu Gln Gln Val Tyr Lys Cys Ala Ala Asp Lys Gln Asp Ala Thr Ile
 260 265 270
 Val Glu Leu Lys Asn Leu Thr Glu Glu Asn Val Lys Lys Glu Asn Arg
 275 280 285
 Arg Gln Asn Val Thr Ile Asp Ile Ile Arg Leu Tyr Ser Ile Gly Gly
 290 295 300
 His Glu Val Pro Phe Gly Asn Ile Thr Leu Pro Ala Asp Ser Glu Ala
 305 310 315 320
 Arg Lys Ala Ala Ile Lys Phe Ile Lys Phe Ile Asn Pro Lys Ile Asn
 325 330 335
 Asp Gly Gln Ile Arg His Ile Pro Val Arg Val Tyr Lys Asn Gly Leu
 340 345 350
 Cys Asp Val Pro His Ile Leu Lys Asp Ile Lys Tyr Gly Lys Asn Ser
 355 360 365
 Gly Glu Lys Leu Val Ala Val Leu Asn
 370 375

<210> 7

<211> 1122

<212> DNA

<213> *Saccharomyces cerevisiae*

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 1 5

gag ggc gtt ccc att cct gaa ttg gaa gaa gga ttc gta ttg att aag 96
 Glu Gly Val Pro Ile Pro Glu Leu Glu Glu Gly Phe Val Leu Ile Lys 30
 15 20 25

aca ctc gct gtt gct ggt aac ccg act gat tgg gca cac att gac tac 144
 Thr Leu Ala Val Ala Gly Asn Pro Thr Asp Trp Ala His Ile Asp Tyr 45
 35 40

aag gtc ggg cct caa gga tct att ctg gga tgt gac gct gcc ggc caa 192
 Lys Val Gly Pro Gln Gly Ser Ile Leu Gly Cys Asp Ala Ala Gly Gln 60
 50 55

att gtc aaa ttg ggc cca gcc gtc gat cct aaa gac ttt tct att ggt 240
 Ile Val Lys Leu Gly Pro Ala Val Asp Pro Lys Asp Phe Ser Ile Gly 75
 65 70

gat tat att tat ggg ttc att cac gga tct tcc gta agg ttt cct tcc 288
 Asp Tyr Ile Tyr Gly Phe Ile His Gly Ser Ser Val Arg Phe Pro Ser 90
 80 85

aat ggt gct ttt gct gaa tat tct gct att tca act gtg gtt gcc tac 336
 Asn Gly Ala Phe Ala Glu Tyr Ser Ala Ile Ser Thr Val Val Ala Tyr 110
 95 100 105

aaa tca ccc aat gaa ctc aaa ttt ttg ggt gaa gat gtt cta cct gcc 384
 Lys Ser Pro Asn Glu Leu Lys Phe Leu Gly Glu Asp Val Leu Pro Ala 125
 115 120

ggc cct gtc agg tct ttg gaa ggg gca gcc act atc cca gtg tca ctg 432
 Gly Pro Val Arg Ser Leu Glu Gly Ala Ala Thr Ile Pro Val Ser Leu 140
 130 135

acc aca gct ggc ttg gtg ttg acc tat aac ttg ggc ttg aac ctg aag 480
 Thr Thr Ala Gly Leu Val Leu Thr Tyr Asn Leu Gly Leu Asn Leu Lys 155
 145 150

tgg gag cca tca acc cca caa aga aac ggc ccc atc tta tta tgg ggc 528
 Trp Glu Pro Ser Thr Pro Gln Arg Asn Gly Pro Ile Leu Leu Trp Gly 170
 160 165

ggt gca act gca gta ggt cag tcg ctc atc caa tta gcc aat aaa ttg 576
 Gly Ala Thr Ala Val Gly Gln Ser Leu Ile Gln Leu Ala Asn Lys Leu 190
 175 180 185

aat ggc ttc acc aag atc att gtt gtg gct tct cgg aaa cac gaa aaa 624
 Asn Gly Phe Thr Lys Ile Ile Val Val Ala Ser Arg Lys His Glu Lys 205
 195 200

ctg ttg aaa gaa tat ggt gct gat caa cta ttt gat tac cat gat att 672
 Leu Leu Lys Glu Tyr Gly Ala Asp Gln Leu Phe Asp Tyr His Asp Ile
 210 215 220

 gac gtg gta gaa caa att aaa cac aag tac aac aat atc tcg tat tta 720
 Asp Val Val Glu Gln Ile Lys His Lys Tyr Asn Asn Ile Ser Tyr Leu
 225 230 235

 gtc gac tgt gtc gcg aat caa aat acg ctt caa caa gtg tac aaa tgt 768
 Val Asp Cys Val Ala Asn Gln Asn Thr Leu Gln Gln Val Tyr Lys Cys
 240 245 250

 gcg gcc gat aaa cag gat gct acc gtt gtc gaa tta act aat ttg aca 816
 Ala Ala Asp Lys Gln Asp Ala Thr Val Val Glu Leu Thr Asn Leu Thr
 255 260 265 270

 gaa gaa aac gtc aaa aag gag aat agg agg caa aat gtc act att gac 864
 Glu Glu Asn Val Lys Lys Glu Asn Arg Arg Gln Asn Val Thr Ile Asp
 275 280 285

 A2 aga aca aga ctg tat tca ata ggc ggc cat gaa gta cca ttt ggt ggc 912
 Arg Thr Arg Leu Tyr Ser Ile Gly Gly His Glu Val Pro Phe Gly Gly
 290 295 300

 att act ttc cct gct gac cca gaa gcc agg aga gct gcc acc gaa ttc 960
 Ile Thr Phe Pro Ala Asp Pro Glu Ala Arg Arg Ala Ala Thr Glu Phe
 305 310 315

 gtc aag ttc atc aat cca aag att agt gat ggg caa att cac cat att 1008
 Val Lys Phe Ile Asn Pro Lys Ile Ser Asp Gly Gln Ile His His Ile
 320 325 330

 cca gca agg gtc tat aag aac ggg ctt tac gat gtt cct cgt atc ctg 1056
 Pro Ala Arg Val Tyr Lys Asn Gly Leu Tyr Asp Val Pro Arg Ile Leu
 335 340 345 350

 gaa gac att aaa atc ggt aag aac tct ggt gaa aaa ctc gtt gcc gta 1104
 Glu Asp Ile Lys Ile Gly Lys Asn Ser Gly Glu Lys Leu Val Ala Val
 355 360 365

 tta aac taatctagaa ac 1122
 Leu Asn

<210> 8
 <211> 368
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 8
 Met Lys Ala Val Val Ile Glu Asp Gly Lys Ala Val Val Lys Glu Gly
 1 5 10 15
 Val Pro Ile Pro Glu Leu Glu Glu Gly Phe Val Leu Ile Lys Thr Leu
 20 25 30
 Ala Val Ala Gly Asn Pro Thr Asp Trp Ala His Ile Asp Tyr Lys Val

35 40 45
 Gly Pro Gln Gly Ser Ile Leu Gly Cys Asp Ala Ala Gly Gln Ile Val
 50 55 60
 Lys Leu Gly Pro Ala Val Asp Pro Lys Asp Phe Ser Ile Gly Asp Tyr
 65 70 75 80
 Ile Tyr Gly Phe Ile His Gly Ser Ser Val Arg Phe Pro Ser Asn Gly
 85 90 95
 Ala Phe Ala Glu Tyr Ser Ala Ile Ser Thr Val Val Ala Tyr Lys Ser
 100 105 110
 Pro Asn Glu Leu Lys Phe Leu Gly Glu Asp Val Leu Pro Ala Gly Pro
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 Val Arg Ser Leu Glu Gly Ala Ala Thr Ile Pro Val Ser Leu Thr Thr
 130 135 140
 Ala Gly Leu Val Leu Thr Tyr Asn Leu Gly Leu Asn Leu Lys Trp Glu
 145 150 155 160
 Pro Ser Thr Pro Gln Arg Asn Gly Pro Ile Leu Leu Trp Gly Gly Ala
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 Thr Ala Val Gly Gln Ser Leu Ile Gln Leu Ala Asn Lys Leu Asn Gly
 180 185 190
 Phe Thr Lys Ile Ile Val Val Ala Ser Arg Lys His Glu Lys Leu Leu
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 Lys Glu Tyr Gly Ala Asp Gln Leu Phe Asp Tyr His Asp Ile Asp Val
 210 215 220
 Val Glu Gln Ile Lys His Lys Tyr Asn Asn Ile Ser Tyr Leu Val Asp
 225 230 235 240
 Cys Val Ala Asn Gln Asn Thr Leu Gln Gln Val Tyr Lys Cys Ala Ala
 245 250 255
 Asp Lys Gln Asp Ala Thr Val Val Glu Leu Thr Asn Leu Thr Glu Glu
 260 265 270
 Asn Val Lys Lys Glu Asn Arg Arg Gln Asn Val Thr Ile Asp Arg Thr
 275 280 285
 Arg Leu Tyr Ser Ile Gly Gly His Glu Val Pro Phe Gly Gly Ile Thr
 290 295 300
 Phe Pro Ala Asp Pro Glu Ala Arg Arg Ala Ala Thr Glu Phe Val Lys
 305 310 315 320
 Phe Ile Asn Pro Lys Ile Ser Asp Gly Gln Ile His His Ile Pro Ala
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ttgatttggg gtgggtgctac agcagtgggt caacaactaa tccaagttgc caaacatata	420
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